

SEQUENCE LISTING

jc971 U.S. PTO
09/813214
03/20/01

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: TUCKER, KENNETH
PLOSILA, LAURA
- (ii) TITLE OF INVENTION: MORAXELLA CATARRHALIS OUTER MEMBRANE
PROTEIN-106 POLYPEPTIDE, GENE SEQUENCE AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 19
- 10 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: PENNIE & EDMONDS
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10036-2711
- 15 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- 20 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Baldwin, Geraldine F.
(B) REGISTRATION NUMBER: 31,232
(C) REFERENCE/DOCKET NUMBER: 7969-060
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 790-9090
(B) TELEFAX: (212) 869-8864
(C) TELEX: 66141 PENNIE
- 25 (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown
- 30 (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- 35 Ile Gly Ile Ser Glu Ala Asp Gly Gly Lys Gly Gly Ala Asn Ala Arg
1 5 10 15
Gly Asp Lys Ser Ile Ala Ile Gly Asp Ile Ala Gln Ala Leu Gly Ser
20 25 30

Gln Ser Ile Ala Ile Gly Asp Asn Lys Ile Val
35 40

(2) INFORMATION FOR SEQ ID NO:2:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly Thr Val Leu Gly Gly Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:3:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "probe"

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGNACNGTNC TGGGNGGNAA RAAR

24

(2) INFORMATION FOR SEQ ID NO:4:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

30 (ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAA GCG GAC GGG GGG AAA GGC GGA GCC AAT GCG CGC GGT GAT AAA TCC
Glu Ala Asp Gly Gly Lys Gly Gly Ala Asn Ala Arg Gly Asp Lys Ser
35 1 5 10 15

48

ATT GCT ATT GGT GAC ATT GCG CAA
Ile Ala Ile Gly Asp Ile Ala Gln
20

72

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

5

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Glu Ala Asp Gly Gly Lys Gly Gly Ala Asn Ala Arg Gly Asp Lys Ser
1 5 10 15

Ile Ala Ile Gly Asp Ile Ala Gln
20

10

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

15

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "probe"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

20 YTTYTTNCCN CCNAGNACNG TNCC

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

25

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = ""probe""

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

30

GGNACNGTNT TRGGNGGNAA RAAR

24

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

35

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = ""probe""

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 YTTYTTNCCN CCYAANACNG TNCC

24

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9542 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

	CTATTGACTT AAATCACCAT ATGGTTATAA TTTAGCATAA TGGTAGGCTT TTTGTAAAAA	60
	TCACATCGCA ATATTGTTTT ACTGTTACTA CCATGCTTGA ATGACGATCC AAATCACCAG	120
15	ATTCATTCAA GTGATGTGTT TGTATACGCA CCATTTACCC TAATTATTTT AATCAAATGC	180
	CTATGTCAGC ATGTATCATT TTTAAGGTA AACCACCATG AATCACATCT ATAAAGTCAT	240
	CTTTAACAAA GCCACAGGCA CATTTATGGC CGTGGCGGAA TATGCCAAAT CCCACAGCAC	300
	GGGGGGGGGT AGCTGTGCTA CAGGGCAAGT TGGCAGTGTA CGCACTCTGA GCTTTGCCCCG	360
20	TATTGCCGCG CTCGCTGTCC TCGTGATCGG TGCACGCTC AATGGCAGTG CTTATGCAGG	420
	TATCGGAATT AGTGAAGCAG ACGGGGGAAA AGGCGGAGCC AATGCGCGCG GTGATAAATC	480
	CATTGCTATT GGTGATATTG CTCAGGCACT TGGCTCTCAA TCTATTGCTA TCGGTGACAA	540
	CAAAATAGTT CATAATTCAA ATAATAATGC TAATATAGGT GCCAAAGCCT CAGGTAATGA	600
	GTCCATCGCC ATCGGTGGTG ATGTATTGGC TTCTGGTCAT GCCTCGATTG CCATCGGTAG	660
25	TGATGACTTA TATTTGAAAA AGGAAACGGT ACAGCAAATC TCAGAGCTTC TACCTATTAT	720
	TCGCGGACAG AAAGCATTAA ACGATATATA CCAACTAGCT GACACTAATC TTCAAAAATA	780
	TAGACGCACA CACGCACAGG GACACGCCAG TACTGCAGTG GGAGCCATGT CATATGCAAA	840
	GGGTCATTTT TCCAACGCCT TTGGTACACG GGCAACAGCT GAAGGTACCT ATTCCTTGGC	900
30	AGTGGGTCTT ACCGCCACAG CCAAAGCAGC ATCTTCAATC GCTGTTGGTT CTAATGCACA	960
	AGCTATCGGG TTTGCAGCGA CAGCCGTTGG TGGAAGTACT CAAGTTAATT TGAATCGAGG	1020
	TATTGCCCTA GGTTTTGGTT CTCAGGTCCT TCAGAAGGAT AATGATGTAA ATGCAGCAAA	1080
	TGTACGGGCC TATGCACCAG ATGATAACCA GCCAATAGAC AACCGGTATA AAGCCACCTT	1140
	CAAGAATGGT GCTACGGATG TATTTTCCAT TGTAATAGT AATGGGAATG ACAGTATCAG	1200
35	GCGTAAATC ATCAATGTCG GTGCAGGTTT TCGGATACC GATGCGGTCA ATGTGGCACA	1260
	GCTTAAAGAG GCGGTGAGGC TGGCTAATCG TCAAATTACT TTTAAGGGTG ATGATAGCAA	1320

	TAATAGAGTA	GAAAAAGGTT	TGGGCAAGAC	TTTAACTATC	ACAGGTGGTG	CACAGACCAG	1380
	CGCATTAAACC	GATCATAACA	TCGGTGTGGT	ACAAAATGGC	GATGGTCTGA	AAGTTCAACT	1440
	TGCTGAAACT	TTAACCAGCC	TTAAAATGGT	TACCACTGAA	AACCTAACCG	CCAACGAGAA	1500
	AGTTACCGTA	GGCAAAACCC	GCCTTACCAC	AGATAAAATT	GGTTTTACCA	ATGATATGAA	1560
5	TGGCATTGAT	GAAAGCAAAC	CTTATCTTGA	TAAAGACACT	GGCATTTCATG	CAGGTGGTCA	1620
	AAAGATTACC	AAACTTACTG	CTGGTGTAGT	AGATGACGAT	GCGGCAACTT	ATGGACAGCT	1680
	TAAAAAAGTT	AACCAAACCG	CTGAAAGTGC	TCTACAAACC	TTTACCGTTA	AAAAGGTAGA	1740
	TAAAAATGGT	AATGATGCTA	ATGACAGCAA	AATCATCACC	GTGGGTAAAA	ATAACAAACC	1800
10	AGACGGTACT	CAAGTCAACA	CCCTAAAACT	CAAAGGTGAA	AACGGTGTTG	ATGTTACAAC	1860
	CGAAACAAAT	GGTACAGTTA	CCTTTGGGCT	TAACCAAAT	AACGGTCTGA	CCGTTGGCAA	1920
	CAGCACCCCTA	AACAACGATG	GCTTATCTGT	TAAAAACACC	AATAGTAACA	AACAAATCCA	1980
	AGTCGGTGCT	GATGGCATT	CATTTACTGA	TATCAGCAAT	AGTAAGCCAG	GTGCTGGCAT	2040
	TGAAAATACC	ACTCGCATT	CCAGAGACGG	TATTGGTTTT	GCTAATAATA	CTGGTTCATT	2100
15	GGATGCAAAC	AAACCCCGCC	TAACCCCAAC	TGGCATTAAAC	GCAGGTGGTA	AAGAGCTGAC	2160
	CAATGTCCAA	TCTGCCATTA	ACCCTGCTAC	CAATGGTGGG	CAGCTAGACT	TTATGAACCG	2220
	CCTAAGCACT	GCTAATACCG	AAAAATCAGG	CTCTGCCGCC	ACCATTAAAG	ACTTATACAA	2280
	CCTATCACAA	GTACCGCTGA	CCTTTGCAGG	TGATACAGGT	CCTAATGTCA	CCAAAAAACT	2340
20	GGGCGAGATT	TTAAAGGTTA	AAGGTGGTAA	AACCACAGCT	GATGATTTAA	CCAAAAATAA	2400
	CATCGGTGTG	GTGGCTGATA	GTACCGATAA	TAGCTTAACC	GTTAAACTTG	CTAAAACTTT	2460
	AAGCGATCTT	GATGCGGTTA	ATACTAAAAC	CCTAAGTACC	AGCGATAAAG	TTACCGTAGA	2520
	CAGTGGAAC	AACACCGCTA	AGCTACAAAA	TGGTGATTTA	ACCTTTAGCA	AACAAAATAC	2580
	AGGTGCTACC	CCTGCCACCA	ACAGCAAAAC	CATCTATGGC	GTTGATGGCT	TGAAGTTTAC	2640
25	TGATAACAAT	GGTATAGCAC	TTGACGGCAC	AACTTACATC	ACCAAAGACA	AAGTTGGCTT	2700
	TGCTAAGCAA	GATGGTTCAC	TTGATAAAAG	CAAACCTTAT	CTTGATAAGG	ACAAGCTAAA	2760
	AGTGGGTGAA	GTTGAGATTA	CCACCAACGG	CATTAATGCA	GGTGGTAAAG	CCATCACAGG	2820
	ACTAAGCAAT	ACCCTAACCG	ATGCCACCAA	CGCAACAACA	GGGCATGTAA	CTCAATTGGG	2880
30	TATCGTTGAT	AGTACTGACA	AAACCCGTGC	CGCCAGCATT	GGTGATGTGC	TAAACGCAGG	2940
	CTTTAACCTA	AAAAATAATG	GTGACGCCAA	AGACTTTGTC	TCCACTTATG	ACACTGTTGA	3000
	TTTTATCAAT	GGCAATGCCA	CCACCGCTAA	AGTCACTTAT	GATGGCAAAG	CCAGTAAAGT	3060
	GGCGTATGAT	GTCAATGTGG	ATGGTACAAC	CATTCATCTA	ACAGGCGCTG	ATGGCAATAA	3120
	AAACCAAATT	GGCGTAAAAA	CCACCACACT	GACCAAAACA	GATGCTAAAG	GTGATAAAGC	3180
35	AATTAACTTT	AGTGTTAACT	CTGGTGATGA	CAAAGCCCTT	ATTAACGCCA	AAGACATCGC	3240
	CGACAATCTA	AACACCCTAG	CTGGTGAAAT	TCGCAACACC	AAAGGCACAG	CAGACACCGC	3300

	CCTACAAACC TTTCAAGTCA AAAAAGTCAA AGAAAATGGT GATGATGATA ATGACGCTGA	3360
	CACCATCACC GTGGGTAAAG ATGCAAAAAC CAATCAAGTC AACACCCTAA AACTCAAAGG	3420
	TAAAAACGGT CTTGATATTC AAACCAATAA AGATGGTACG GTTACCTTTG GCATTAACAC	3480
	CCAAAGCGGT CTTAAAGCCG GCAACAACAC CACTCTAAAC AACAATGGCT TGTCTATTAA	3540
5	AAACACCGCT GGTAACGAAC AAATCCAAGT CGGTGCTGAT GGCGTGAAGT TTGCCAAGGT	3600
	TAATAATGGT GTTGTAGGTG CTGGCATTGA TGGCACAACCT CGCATTACCA GAGATGAAAT	3660
	TGGCTTTGCT GGGACTAATG GCTCACTTGA TAAAAGCAAA CCCCACCTAA GCAAAGACGG	3720
	CATTAACGCA GGTGGTAAAA AGATTACCAA CATTCAATCA GGTGAGATTG CCAAAAACAG	3780
10	CAATGATGCT GTGACAGGCG GCAAGATTTA TGATTTAAAA ACCGAACTTG AAAACAAAAT	3840
	CAGCAGTACT GCCAAAACAG CACAAAACCTC ATTACACGAA TTCTCAGTAG CAGATGAACA	3900
	AGGTAATAAC TTTACGGTTA GTAACCTTA CTCCAGTTAT GACACCTCAA AGACCTCTGA	3960
	TGTCATCACC TTTGCAGGTG AAAACGGCAT TACCACCAAG GTAAATAAAG GTGTGGTGCG	4020
	TGTGGGCATT GACCAAACCA AAGGCTTAAC CACGCCTAAG CTGACCGTGG GTAATAATAA	4080
15	TGGCAAAGGC ATTGTCATTG ACAGCCAAAA TGGTCAAAAT ACCATCACAG GACTAAGCAA	4140
	CACTCTAGCT AATGTTACCA ATGATAAAGG TAGCGTACGC ACCACAGAAC AGGGCAAGAT	4200
	AATCAAAGAC GAAGACAAAA CCCGTGCCGC CAGCATTTGT GATGTGCTAA GCGCAGGCTT	4260
	TAAGTTGCAA GGCAATGGTG AAGCGGTTGA CTTTGTCTCC ACTTATGACA CTGTCAACTT	4320
20	TGCCGATGGC AATGCCACCA CCGCTAAGGT GACCTATGAT GACACAAGCA AAACCAGTAA	4380
	AGTGGTCTAT GATGTCAATG TGGATGATAC AACCATTGAA GTTAAAGATA AAAAAGTTGG	4440
	CGTAAAAACC ACCACATTGA CCAGTACTGG CACAGGTGCT AATAAATTTG CCCTAAGCAA	4500
	TCAAGCTACT GGCGATGCGC TTGTCAAGGC CAGTGATATC GTTGCTCATC TAAACACCTT	4560
	ATCTGGCGAC ATCCAAACTG CCAAAGGGGC AAGCCAAGCG AACAGCTCAG CAGGCTATGT	4620
25	GGATGCTGAT GGCAATAAGG TCATCTATGA CAGTACCGAT AACAAGTACT ATCAAGCCAA	4680
	AAATGATGGC ACAGTTGATA AAACCAAAGA AGTTGCCAAA GACAAACTGG TCGCCCAAGC	4740
	CCAAACCCCA GATGGCACAT TGGCTCAAAT GAATGTCAAA TCAGTCATTA ACAAAGAACA	4800
	AGTAAATGAT GCCAATAAAA AGCAAGGCAT CAATGAAGAC AACGCCTTTG TTAAAGGACT	4860
30	TGAAAAAGCC GCTTCTGATA ACAAACCAA AAACGCCGCA GTAAGTGTGG GTGATTTAAA	4920
	TGCCGTTGCC CAAACACCGC TGACCTTTGC AGGGGATACA GGCACAACGG CTAAAAAACT	4980
	GGGCGAGACT TTGACCATCA AAGGTGGGCA AACAGACACC AATAAGCTAA CCGATAATAA	5040
	CATCGGTGTG GTAGCAGGTA CTGATGGCTT CACTGTCAAA CTTGCCAAAG ACCTAACCAA	5100
	TCTTAACAGC GTTAATGCAG GTGGTACCAA AATTGATGAC AAAGGCGTGT CTTTTGTAGA	5160
35	CTCAAGCGGT CAAGCCAAAG CAAACACCCC TGTGCTAAGT GCCAATGGGC TGGACCTGGG	5220
	TGGCAAGGTC ATCAGCAATG TGGGCAAAG CACAAAAGAC ACCGACGCTG CCAATGTACA	5280

	ACAGTTAAAC GAAGTACGCA ACTTGTTGGG TCTTGGAAT GCTGGTAATG ATAACGCTGA	5340
	CGGCAATCAG GTAAACATTG CCGACATCAA AAAAGACCCA AATTCAGGTT CATCATCTAA	5400
	CCGCACTGTC ATCAAAGCAG GCACGGTACT TGGCGGTAAA GGTAATAACG ATACCGAAAA	5460
	ACTTGCCACT GGTGGTGATC AAGTGGGCGT GGATAAAGAC GGCAACGCTA ACGGCGATTT	5520
5	AAGCAATGTT TGGGTCAAAA CCCAAAAAGA TGGCAGCAA AAAGCCCTGC TCGCCACTTA	5580
	TAACGCCGCA GGTCAGACCA ACTATTTGAC CAACAACCCC GCAGAAGCCA TTGACAGAAT	5640
	AAATGAACAA GGTATCCGCT TCTTCCATGT CAACGATGGC AATCAAGAGC CTGTGGTACA	5700
	AGGGCGTAAC GGCATTGACT CAAGTGCCTC AGGCAAGCAC TCAGTGGCGA TAGGTTTCCA	5760
10	GGCCAAGGCA GATGGTGAAG CCGCCGTTGC CATAGGCAGA CAAACCCAAG CAGGCAACCA	5820
	ATCCATCGCC ATCGGTGATA ACGCACAAGC CACAGGCGAT CAATCCATCG CCATCGGTAC	5880
	AGGCAATGTG GTAGCAGGTA AGCACTCTGG TGCCATCGGC GACCCAAGCA CTGTTAAGGC	5940
	TGATAACAGT TACAGTGTGG GTAATAACAA CCAGTTTACC GATGCCACTC AAACCGATGT	6000
	CTTTGGTGTG GGCAATAACA TCACCGTGAC CGAAAGTAAC TCGGTTGCCT TAGGTTCAAA	6060
15	CTCTGCCATC AGTGCAGGCA CACACGCAGG CACACAAGCC AAAAAATCTG ACGGCACAGC	6120
	AGGTACAACC ACCACAGCAG GTGCAACCGG TACGGTTAAA GGCTTTGCTG GACAAACGGC	6180
	GGTTGGTGCG GTCTCCGTGG GTGCCTCAGG TGCTGAACGC CGTATCCAAA ATGTGGCAGC	6240
	AGGTGAGGTC AGTGCCACCA GCACCGATGC GGTCAATGGT AGCCAGTTGT ACAAAGCCAC	6300
20	CCAAGGCATT GCCAACGCAA CCAATGAGCT TGACCATCGT ATCCACCAA ACGAAAATAA	6360
	AGCCAATGCA GGGATTTTCAT CAGCGATGGC GATGGCGTCC ATGCCACAAG CCTACATTCC	6420
	TGGCAGATCC ATGGTTACCG GGGGTATTGC CACCCACAAC GGTCAAGGTG CGGTGGCAGT	6480
	GGGACTGTCTG AAGCTGTCTG ATAATGGTCA ATGGGTATTT AAAATCAATG GTTCAGCCGA	6540
	TACCCAAGGC CATGTAGGGG CGGCAGTTGG TGCAGTTTTT CACTTTTAAG CCATAAATCG	6600
25	CAAGATTTTA CTTAAAAATC AATCTCACCA TAGTTGTATA AAACAGCATC AGCATCAGTC	6660
	ATATTACTGA TGCTGATGTT TTTTATCACT TAAACCATTT TACCGCTCAA GTGATTATCT	6720
	TTCAACATGA CCAAATCGCC ATTGATCATA GGTAAACTTA TTGAGTAAAT TTTATCAATG	6780
	TAGTTGTTAG ATATGGTTAA AATTGTGCCA TTGACCAAAA AATTACCGAT TTATCCCGAA	6840
30	AATTTCTGAT TATGATCACT TTTCATAAAT TTCCCCAATT TGTCTTTATA AATATCCCAA	6900
	GAAATGGTAT TATTTTATTG CCATCAGCAT ATGCGACAAC TCATCGTATC ATCTTTTTAT	6960
	CATAAAAATG CAAATAGGCA TATGCATTTT TTGAATTGAA CTTACGCACT GAGAGATCCC	7020
	CTCATAATTT CCCCAAAGCG TAACCATGTG TGAATAAATT TTGAGCTAGT AGGGTTGCAG	7080
	CCACGAGTAA GTCTTCCCTT GTTATTGTGT AGCCAGAATG CCGCAAACT TCCATGCCTA	7140
35	AGCGAACTGT TGAGAGTACG TTTTCGATTTC TGACTGTGTT AGCCTGGAAG TGCTTGTCCT	7200
	AACCTTGTTT CTGAGCATGA ACGCCCGCAA GCCAACATGT TAGTTGAAGC ATCAGGGCGA	7260

	TTAGCAGCAT GATATCAAAA CGCTCTGAGC TGCTCGTTCG GCTATGGCGT AGGCCTAGTC	7320
	CGTAGGCAGG ACTTTTCAAG TCTCGGAAGG TTTCTTCAAT CTGCATTTCG TTCGAATAGA	7380
	TATTAACAAG TTGTTTGGGT GTTCGAATTT CAACAGGTAA GTTAGTTGCT AGAATCCATG	7440
	GCTCCTTTGC CGACGCTGAG TAGATTTTAG GTGACGGGTG GTGACAATGA GTCCGTGTCTG	7500
5	AGCGCTGATT TTTTCGGCCT TTAGAGCGAG ATTTATACAA TAGAATTTGG CATGAGATTG	7560
	GATTGCTTTT AGTCAGCCTC TTATAGCCTA AAGTCTTTGA GTGACTAGAT GACATATCAT	7620
	GTAAGTTGCT GATAGGTTTC CAGTTTTCCG CTCCTAGGTC TGCATATTGT ACTTTTCCTC	7680
	TTACTCGACT TAACCAGTAC CAACCCAGCT TCTCAACGGA TTTATACCAT GGCACCTTAA	7740
10	AGCCAGCATC ACTGACAATG AGCGGTGTGG TGTACTCGG TAGAATGCTC GCAAGGTCGG	7800
	CTAGAAATTG GTCATGAGCT TTCTTTGAAC ATTGCTCTGA AAGCGGGAAC GCTTTCTCAT	7860
	AAAGAGTAAC AGAACGACCG TGTAGTGC GA CTGAAGCTCG CAATACCATA AGCCGTTTTT	7920
	GCTCACGGAT ATCAGACCAG TCAACAAGTA CAATGGGCAT CGTATTGCCC GAACAGATAA	7980
	AGCTAGCATG CCAACGGTAT ACAGCGAGTC GCTCTTTGTG GAGGTGACGA TTACCTAACA	8040
15	ATCGGTTCGAT TCGTTTGATG TTATGTTTTG TTCTCGCTTT GGTGCGCAGG TTACGGCCAA	8100
	GTTGCGTAAG AGTGAGAGTT TTACAGTCAA GTAAGGCGTG GCAAGCCAAC GTTAAGCTGT	8160
	TGAGTCGTTT TAAGTGTAAT TCGGGGCAGA ATTGGTAAAG AGAGTCGTGT AAAATATCGA	8220
	GTTGCGACAT TTTGTTGTCT GATTATTGAT TTTTGGCGAA ACCATTTGAT CATATGACAA	8280
20	GATGTGTATC TACCTTAACT TAATGATTTT GATAAAAATC ATTAGGGGAT TCATCAGACT	8340
	TACGCATCTT TCATTATGGG AATTAGGTCA GTAATTATGA CAAAAAATTA TGCATTATTA	8400
	TCCGTCTCAG ATAAAACGCA AATCGTTGAA TTTGCCCAAG GTTTGGTAGA ATCTGGCTTT	8460
	GGTATTTTAT CCACAGGTGG TACTTTTAAA CTCTTAAAG AACATGGGAT TGACGCCATT	8520
	GAGGTTTCTG CCCATACAGG TTTTGCTGAA ATGATGGATG GTCGTGTTAA GACCCTACAT	8580
25	CCCAAATTC ATGGTGGTAT TTTGGGCCGT CGTGGCATTG ATGATGCCAT TATGAATGAA	8640
	CATGGCATTG ATCGCATTGA TATCGTTGTC GTGAATTTAT ATCCATTTGC CAACACGGTC	8700
	GCCAAAGACG GTGTTGTTAT GTCTGATGCG ATTGAAAATA TTGATATTGG TGGGCCTGCT	8760
	ATGGTACGCT CAGCCGCCAA AAATCATGCC CATGTTGGTA TTATCACCAG CCCAAATGAC	8820
30	TACTCACGCA TCCTAGATGA ACTAAAAAAC CAAGGTCATT TAAGCCACAA CACTCGTTTT	8880
	GATTTGGCAG TCAAAGCATT TGAACACACT GCCGCCTATG ATGGTATGAT TGCCAGCTGG	8940
	CTAGGTGCAC GCTTACCAGT GGATAAAGAG ACGGCACCCA GTGATGATGC CACTGCAACC	9000
	ACTCAATTTT CACGCACTTT TAATCACCAA TTCACCAAAG CACAAGAGCT TAGATATGGC	9060
	GAAAACCCAC ATCAGTCAGC AGCCTTTTAT GTAGATGATC ATGCAACAGA AGCGTCTGTT	9120
35	GCGACTGCAC AGCAATTACA AGGTAAAGCG TTGTCTTATA ATAATATTGC TGATACCGAT	9180
	GCGGCACTTG AGTGTGTCAA ATCTTTTACC ACGCCTGCTT GTGTGATTGT CAAACATGCC	9240

AATCCTTGTG GTGTTGCAAC ATCAGAAAAC GGTATTTTAG ATGCTTATCA CTTAGCATAT 9300
 GCAACCGATC CTGAATCTGC CTTTGGTGGC ATTATTGCCT TTAACCGAGA ATTAGACAGT 9360
 GATACAGCCC GTACCATCGT TGAGCGTCAA TTTGTTGAAG TCATCATCGC ACCAAGCATC 9420
 GCTGAAGGTG TTCTAGAGCG GCCGCGGGCC CATCGATTTT CCACCCGGGT GGGGTACCAG 9480
 5 GTAAGTGTAC CCAATTCGCC CTATAGTGAG TCGTATTACA ATTCAGTGGC CGTCGTTTTA 9540
 CA 9542

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 2123 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

15 Met Asn His Ile Tyr Lys Val Ile Phe Asn Lys Ala Thr Gly Thr Phe
 1 5 10 15
 Met Ala Val Ala Glu Tyr Ala Lys Ser His Ser Thr Gly Gly Gly Ser
 20 25 30
 Cys Ala Thr Gly Gln Val Gly Ser Val Arg Thr Leu Ser Phe Ala Arg
 35 40 45
 Ile Ala Ala Leu Ala Val Leu Val Ile Gly Ala Thr Leu Asn Gly Ser
 50 55 60
 Ala Tyr Ala Gly Ile Gly Ile Ser Glu Ala Asp Gly Gly Lys Gly Gly
 65 70 75 80
 20 Ala Asn Ala Arg Gly Asp Lys Ser Ile Ala Ile Gly Asp Ile Ala Gln
 85 90 95
 Ala Leu Gly Ser Gln Ser Ile Ala Ile Gly Asp Asn Lys Ile Val His
 100 105 110
 Asn Ser Asn Asn Asn Ala Asn Ile Gly Ala Lys Ala Ser Gly Asn Glu
 115 120 125
 Ser Ile Ala Ile Gly Gly Asp Val Leu Ala Ser Gly His Ala Ser Ile
 130 135 140
 25 Ala Ile Gly Ser Asp Asp Leu Tyr Leu Lys Lys Glu Thr Val Gln Gln
 145 150 155 160
 Ile Ser Glu Leu Leu Pro Ile Ile Arg Gly Gln Lys Ala Leu Asn Asp
 165 170 175
 Ile Tyr Gln Leu Ala Asp Thr Asn Leu Gln Lys Tyr Arg Arg Thr His
 180 185 190
 Ala Gln Gly His Ala Ser Thr Ala Val Gly Ala Met Ser Tyr Ala Lys
 195 200 205
 Gly His Phe Ser Asn Ala Phe Gly Thr Arg Ala Thr Ala Glu Gly Thr
 210 215 220
 30 Tyr Ser Leu Ala Val Gly Leu Thr Ala Thr Ala Lys Ala Ala Ser Ser
 225 230 235 240
 Ile Ala Val Gly Ser Asn Ala Gln Ala Ile Gly Phe Ala Ala Thr Ala
 245 250 255
 Val Gly Gly Ser Thr Gln Val Asn Leu Asn Arg Gly Ile Ala Leu Gly
 260 265 270
 Phe Gly Ser Gln Val Leu Gln Lys Asp Asn Asp Val Asn Ala Ala Asn
 275 280 285
 35 Val Arg Ala Tyr Ala Pro Asp Asp Asn Gln Pro Ile Asp Asn Arg Tyr
 290 295 300
 Lys Ala Thr Phe Lys Asn Gly Ala Thr Asp Val Phe Ser Ile Gly Asn
 305 310 315 320
 Ser Asn Gly Asn Asp Ser Ile Arg Arg Lys Ile Ile Asn Val Gly Ala

					325					330					335	
	Gly	Ser	Ala	Asp	Thr	Asp	Ala	Val	Asn	Val	Ala	Gln	Leu	Lys	Glu	Ala
				340					345					350		
	Val	Arg	Leu	Ala	Asn	Arg	Gln	Ile	Thr	Phe	Lys	Gly	Asp	Asp	Ser	Asn
			355					360					365			
	Asn	Arg	Val	Glu	Lys	Gly	Leu	Gly	Lys	Thr	Leu	Thr	Ile	Thr	Gly	Gly
			370				375					380				
5	Ala	Gln	Thr	Ser	Ala	Leu	Thr	Asp	His	Asn	Ile	Gly	Val	Val	Gln	Asn
	385						390				395				400	
	Gly	Asp	Gly	Leu	Lys	Val	Gln	Leu	Ala	Glu	Thr	Leu	Thr	Ser	Leu	Lys
					405					410				415		
	Met	Val	Thr	Thr	Glu	Asn	Leu	Thr	Ala	Asn	Glu	Lys	Val	Thr	Val	Gly
					420				425					430		
	Lys	Thr	Arg	Leu	Thr	Thr	Asp	Lys	Ile	Gly	Phe	Thr	Asn	Asp	Met	Asn
			435					440					445			
	Gly	Ile	Asp	Glu	Ser	Lys	Pro	Tyr	Leu	Asp	Lys	Asp	Thr	Gly	Ile	His
			450				455					460				
10	Ala	Gly	Gly	Gln	Lys	Ile	Thr	Lys	Leu	Thr	Ala	Gly	Val	Val	Asp	Asp
	465						470				475				480	
	Asp	Ala	Ala	Thr	Tyr	Gly	Gln	Leu	Lys	Lys	Val	Asn	Gln	Thr	Ala	Glu
					485					490				495		
	Ser	Ala	Leu	Gln	Thr	Phe	Thr	Val	Lys	Val	Asp	Lys	Asn	Gly	Asn	
				500					505				510			
	Asp	Ala	Asn	Asp	Ser	Lys	Ile	Ile	Thr	Val	Gly	Lys	Asn	Asn	Lys	Pro
			515					520					525			
15	Asp	Gly	Thr	Gln	Val	Asn	Thr	Leu	Lys	Leu	Lys	Gly	Glu	Asn	Gly	Val
			530				535					540				
	Asp	Val	Thr	Thr	Glu	Thr	Asn	Gly	Thr	Val	Thr	Phe	Gly	Leu	Asn	Gln
	545					550					555				560	
	Asn	Asn	Gly	Leu	Thr	Val	Gly	Asn	Ser	Thr	Leu	Asn	Asn	Asp	Gly	Leu
				565					570					575		
	Ser	Val	Lys	Asn	Thr	Asn	Ser	Asn	Lys	Gln	Ile	Gln	Val	Gly	Ala	Asp
				580					585				590			
	Gly	Ile	Thr	Phe	Thr	Asp	Ile	Ser	Asn	Ser	Lys	Pro	Gly	Ala	Gly	Ile
			595					600					605			
20	Glu	Asn	Thr	Thr	Arg	Ile	Thr	Arg	Asp	Gly	Ile	Gly	Phe	Ala	Asn	Asn
			610				615					620				
	Thr	Gly	Ser	Leu	Asp	Ala	Asn	Lys	Pro	Arg	Leu	Thr	Pro	Thr	Gly	Ile
			625			630					635				640	
	Asn	Ala	Gly	Gly	Lys	Glu	Leu	Thr	Asn	Val	Gln	Ser	Ala	Ile	Asn	Pro
				645					650					655		
	Ala	Thr	Asn	Gly	Gln	Leu	Asp	Phe	Met	Asn	Arg	Leu	Ser	Thr	Ala	
				660				665					670			
25	Asn	Thr	Glu	Lys	Ser	Gly	Ser	Ala	Ala	Thr	Ile	Lys	Asp	Leu	Tyr	Asn
			675					680					685			
	Leu	Ser	Gln	Val	Pro	Leu	Thr	Phe	Ala	Gly	Asp	Thr	Gly	Pro	Asn	Val
			690				695					700				
	Thr	Lys	Lys	Leu	Gly	Glu	Ile	Leu	Lys	Val	Lys	Gly	Gly	Lys	Thr	Thr
			705			710					715				720	
	Ala	Asp	Asp	Leu	Thr	Lys	Asn	Asn	Ile	Gly	Val	Val	Ala	Asp	Ser	Thr
				725					730					735		
	Asp	Asn	Ser	Leu	Thr	Val	Lys	Leu	Ala	Lys	Thr	Leu	Ser	Asp	Leu	Asp
				740				745					750			
30	Ala	Val	Asn	Thr	Lys	Thr	Leu	Thr	Ala	Ser	Asp	Lys	Val	Thr	Val	Asp
			755					760					765			
	Ser	Gly	Asn	Asn	Thr	Ala	Lys	Leu	Gln	Asn	Gly	Asp	Leu	Thr	Phe	Ser
			770				775					780				
	Lys	Gln	Asn	Thr	Gly	Ala	Thr	Pro	Ala	Thr	Asn	Ser	Lys	Thr	Ile	Tyr
			785			790					795				800	
	Gly	Val	Asp	Gly	Leu	Lys	Phe	Thr	Asp	Asn	Asn	Gly	Ile	Ala	Leu	Asp
				805					810					815		
35	Gly	Thr	Thr	Tyr	Ile	Thr	Lys	Asp	Lys	Val	Gly	Phe	Ala	Lys	Gln	Asp
				820				825						830		
	Gly	Ser	Leu	Asp	Lys	Ser	Lys	Pro	Tyr	Leu	Asp	Lys	Asp	Lys	Leu	Lys
			835					840					845			
	Val	Gly	Glu	Val	Glu	Ile	Thr	Thr	Asn	Gly	Ile	Asn	Ala	Gly	Gly	Lys

	850		855		860
	Ala Ile Thr Gly Leu Ser Asn Thr Leu Thr Asp Ala Thr Asn Ala Thr				
	865		870		875
	Thr Gly His Val Thr Gln Leu Gly Ile Val Asp Ser Thr Asp Lys Thr				880
		885		890	
	Arg Ala Ala Ser Ile Gly Asp Val Leu Asn Ala Gly Phe Asn Leu Lys				895
		900		905	
5	Asn Asn Gly Asp Ala Lys Asp Phe Val Ser Thr Tyr Asp Thr Val Asp				910
		915		920	
	Phe Ile Asn Gly Asn Ala Thr Thr Ala Lys Val Thr Tyr Asp Gly Lys				925
		930		935	
	Ala Ser Lys Val Ala Tyr Asp Val Asn Val Asp Gly Thr Thr Ile His				940
		945		950	
	Leu Thr Gly Ala Asp Gly Asn Lys Asn Gln Ile Gly Val Lys Thr Thr				955
		965		970	
	Thr Leu Thr Lys Thr Asp Ala Lys Gly Asp Lys Ala Ile Asn Phe Ser				975
		980		985	
10	Val Asn Ser Gly Asp Asp Lys Ala Leu Ile Asn Ala Lys Asp Ile Ala				990
		995		1000	
	Asp Asn Leu Asn Thr Leu Ala Gly Glu Ile Arg Asn Thr Lys Gly Thr				1005
		1010		1015	
	Ala Asp Thr Ala Leu Gln Thr Phe Gln Val Lys Lys Val Lys Glu Asn				1020
		1025		1030	
	Gly Asp Asp Asp Asn Asp Ala Asp Thr Ile Thr Val Gly Lys Asp Ala				1035
		1045		1050	
15	Lys Thr Asn Gln Val Asn Thr Leu Lys Leu Lys Gly Lys Asn Gly Leu				1055
		1060		1065	
	Asp Ile Gln Thr Asn Lys Asp Gly Thr Val Thr Phe Gly Ile Asn Thr				1070
		1075		1080	
	Gln Ser Gly Leu Lys Ala Gly Asn Asn Thr Thr Leu Asn Asn Asn Gly				1085
		1090		1095	
	Leu Ser Ile Lys Asn Thr Ala Gly Asn Glu Gln Ile Gln Val Gly Ala				1100
		1105		1110	
	Asp Gly Val Lys Phe Ala Lys Val Asn Asn Gly Val Val Gly Ala Gly				1115
		1125		1130	
20	Ile Asp Gly Thr Thr Arg Ile Thr Arg Asp Glu Ile Gly Phe Ala Gly				1135
		1140		1145	
	Thr Asn Gly Ser Leu Asp Lys Ser Lys Pro His Leu Ser Lys Asp Gly				1150
		1155		1160	
	Ile Asn Ala Gly Gly Lys Lys Ile Thr Asn Ile Gln Ser Gly Glu Ile				1165
		1170		1175	
	Ala Gln Asn Ser Asn Asp Ala Val Thr Gly Gly Lys Ile Tyr Asp Leu				1180
		1185		1190	
25	Lys Thr Glu Leu Glu Asn Lys Ile Ser Ser Thr Ala Lys Thr Ala Gln				1195
		1205		1210	
	Asn Ser Leu His Glu Phe Ser Val Ala Asp Glu Gln Gly Asn Asn Phe				1215
		1220		1225	
	Thr Val Ser Asn Pro Tyr Ser Ser Tyr Asp Thr Ser Lys Thr Ser Asp				1230
		1235		1240	
	Val Ile Thr Phe Ala Gly Glu Asn Gly Ile Thr Thr Lys Val Asn Lys				1245
		1250		1255	
	Gly Val Val Arg Val Gly Ile Asp Gln Thr Lys Gly Leu Thr Thr Pro				1260
		1265		1270	
30	Lys Leu Thr Val Gly Asn Asn Asn Gly Lys Gly Ile Val Ile Asp Ser				1275
		1285		1290	
	Gln Asn Gly Gln Asn Thr Ile Thr Gly Leu Ser Asn Thr Leu Ala Asn				1295
		1300		1305	
	Val Thr Asn Asp Lys Gly Ser Val Arg Thr Thr Glu Gln Gly Lys Ile				1310
		1315		1320	
	Ile Lys Asp Glu Asp Lys Thr Arg Ala Ala Ser Ile Val Asp Val Leu				1325
		1330		1335	
35	Ser Ala Gly Phe Asn Leu Gln Gly Asn Gly Glu Ala Val Asp Phe Val				1340
		1345		1350	
	Ser Thr Tyr Asp Thr Val Asn Phe Ala Asp Gly Asn Ala Thr Thr Ala				1355
		1365		1370	
	Lys Val Thr Tyr Asp Asp Thr Ser Lys Thr Ser Lys Val Val Tyr Asp				1375

1380 1385 1390
 Val Asn Val Asp Asp Thr Thr Ile Glu Val Lys Asp Lys Lys Leu Gly
 1395 1400 1405
 Val Lys Thr Thr Thr Leu Thr Ser Thr Gly Thr Gly Ala Asn Lys Phe
 1410 1415 1420
 Ala Leu Ser Asn Gln Ala Thr Gly Asp Ala Leu Val Lys Ala Ser Asp
 425 1430 1435 1440
 5 Ile Val Ala His Leu Asn Thr Leu Ser Gly Asp Ile Gln Thr Ala Lys
 1445 1450 1455
 Gly Ala Ser Gln Ala Asn Ser Ser Ala Gly Tyr Val Asp Ala Asp Gly
 1460 1465 1470
 Asn Lys Val Ile Tyr Asp Ser Thr Asp Asn Lys Tyr Tyr Gln Ala Lys
 1475 1480 1485
 Asn Asp Gly Thr Val Asp Lys Thr Lys Glu Val Ala Lys Asp Lys Leu
 1490 1495 1500
 Val Ala Gln Ala Gln Thr Pro Asp Gly Thr Leu Ala Gln Met Asn Val
 505 1510 1515 1520
 10 Lys Ser Val Ile Asn Lys Glu Gln Val Asn Asp Ala Asn Lys Lys Gln
 1525 1530 1535
 Gly Ile Asn Glu Asp Asn Ala Phe Val Lys Gly Leu Glu Lys Ala Ala
 1540 1545 1550
 Ser Asp Asn Lys Thr Lys Asn Ala Ala Val Thr Val Gly Asp Leu Asn
 1555 1560 1565
 Ala Val Ala Gln Thr Pro Leu Thr Phe Ala Gly Asp Thr Gly Thr Thr
 1570 1575 1580
 15 Ala Lys Lys Leu Gly Glu Thr Leu Thr Ile Lys Gly Gly Gln Thr Asp
 585 1590 1595 1600
 Thr Asn Lys Leu Thr Asp Asn Asn Ile Gly Val Val Ala Gly Thr Asp
 1605 1610 1615
 Gly Phe Thr Val Lys Leu Ala Lys Asp Leu Thr Asn Leu Asn Ser Val
 1620 1625 1630
 Asn Ala Gly Gly Thr Lys Ile Asp Asp Lys Gly Val Ser Phe Val Asp
 1635 1640 1645
 Ser Ser Gly Gln Ala Lys Ala Asn Thr Pro Val Leu Ser Ala Asn Gly
 1650 1655 1660
 20 Leu Asp Leu Gly Gly Lys Val Ile Ser Asn Val Gly Lys Gly Thr Lys
 665 1670 1675 1680
 Asp Thr Asp Ala Ala Asn Val Gln Gln Leu Asn Glu Val Arg Asn Leu
 1685 1690 1695
 Leu Gly Leu Gly Asn Ala Gly Asn Asp Asn Ala Asp Gly Asn Gln Val
 1700 1705 1710
 Asn Ile Ala Asp Ile Lys Lys Asp Pro Asn Ser Gly Ser Ser Ser Asn
 1715 1720 1725
 25 Arg Thr Val Ile Lys Ala Gly Thr Val Leu Gly Gly Lys Gly Asn Asn
 1730 1735 1740
 Asp Thr Glu Lys Leu Ala Thr Gly Gly Val Gln Val Gly Val Asp Lys
 745 1750 1755 1760
 Asp Gly Asn Ala Asn Gly Asp Leu Ser Asn Val Trp Val Lys Thr Gln
 1765 1770 1775
 Lys Asp Gly Ser Lys Lys Ala Leu Leu Ala Thr Tyr Asn Ala Ala Gly
 1780 1785 1790
 Gln Thr Asn Tyr Leu Thr Asn Asn Pro Ala Glu Ala Ile Asp Arg Ile
 1795 1800 1805
 30 Asn Glu Gln Gly Ile Arg Phe Phe His Val Asn Asp Gly Asn Gln Glu
 1810 1815 1820
 Pro Val Val Gln Gly Arg Asn Gly Ile Asp Ser Ser Ala Ser Gly Lys
 825 1830 1835 1840
 His Ser Val Ala Ile Gly Phe Gln Ala Lys Ala Asp Gly Glu Ala Ala
 1845 1850 1855
 Val Ala Ile Gly Arg Gln Thr Gln Ala Gly Asn Gln Ser Ile Ala Ile
 1860 1865 1870
 35 Gly Asp Asn Ala Gln Ala Thr Gly Asp Gln Ser Ile Ala Ile Gly Thr
 1875 1880 1885
 Gly Asn Val Val Ala Gly Lys His Ser Gly Ala Ile Gly Asp Pro Ser
 1890 1895 1900
 Thr Val Lys Ala Asp Asn Ser Tyr Ser Val Gly Asn Asn Asn Gln Phe

Ser Gln Ser Ile Ala Ile Gly Asp
 35 40

(2) INFORMATION FOR SEQ ID NO:13:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10 Glu Ala Asp Gly Gly Lys Gly Gly Ala Asn Ala Arg Gly Asp Lys Ser
 1 5 10 15
 Ile Ala Ile Gly Asp Ile Ala Gln
 20

(2) INFORMATION FOR SEQ ID NO:14:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

20 Gly Ala Arg Gly Cys Asn Gly Ala Tyr Gly Gly Asn Gly Gly Asn Ala
 1 5 10 15
 Ala Arg

(2) INFORMATION FOR SEQ ID NO:15:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

30 Tyr Thr Gly Asn Gly Cys Asp Ala Thr Arg Thr Cys Asn Cys Cys Asp
 1 5 10 15
 Ala Thr

(2) INFORMATION FOR SEQ ID NO:16:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAAGCGGACG GGGGAAA

18

(2) INFORMATION FOR SEQ ID NO:17:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

10 TTGCGCAATG TCACCAAT

18

(2) INFORMATION FOR SEQ ID NO:18:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAAGCGGACG GGGGGAAAGG CGGAGCCAAT GCGCGCGGTG ATAAATCCAT TGCTATTGGT

60

20 GACATTGCGC AA

72

(2) INFORMATION FOR SEQ ID NO:19:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Glu Ala Asp Gly Gly Lys Gly Gly Ala Asn Ala Arg Gly Asp Lys Ser
1 5 10 15

30 Ile Ala Ile Gly Asp Ile Ala Gln
20

35